

Figure 1

## CDRH2

1.	50	<b>GINPNNVGSI<u>Y</u>NQKFRG</b>	66	708
	254	<b>NITVNNSGS<u>T</u>CAHNS</b>	290	CEA
	288	<b>NITVNNSGS<u>Y</u>MCQAHNS</b>	304	NCA
2.	50	<b>GINPNNVGSI<u>Y</u>NQKFRG</b>	66	708
	610	<b>KITPNNNGT<u>Y</u>ACFVSNL</b>	626	CEA
	288	<b>NITVNNSGS<u>Y</u>MCQAHNS</b>	304	NCA
3.	50	<b>GINPNNVGSI<u>Y</u>NQKFRG</b>	66	708
	629	<b>GRNN<u>S</u>IVKSITVSASGT</b>	645	CEA

## CDRH3

1	100	<b>GY<u>G</u>NYVAY</b>	107	708
	30	<b>GY<u>S</u>WYKGE</b>	37	CEA
	59	<b>GY<u>S</u>WYKGE</b>	72	NCA
2.	100	<b>GY<u>G</u>NYVAY</b>	107	708
	389	<b>SY<u>T</u>YYRPG</b>	396	CEA
	242	<b>SKAN<u>Y</u>RPG</b>	255	NCA
3.	100	<b>GY<u>G</u>NYVAY</b>	107	708
	480	<b>EDKDAVA<u>F</u></b>	487	CEA
	159	<b>EDKDAVA<u>F</u></b>	165	NCA

**Figure 2****CDRH2**

HLA-A3	NVGSIYNQK IVKSITVSA	708 CEA
Pan DR	INPNNVGSI SIVKSITVSA	708 CEA
HLA-DR1	VGSIYNQKF SIVKSITVS	708 CEA
HLA-DR1	INPNNVGSI LATRNNNSI	708 CEA
HLA-DR7	VGSIYN IVKSITV	708 CEA

**CDRH3**

HLA-A3	CARGYGNYY HLFGYSWYK NRFGYSWYK	708 CEA NCA
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**Figure 3****A:**

1            10            20            30            40            50            60            70  
EVQLQQSGPELVKPGASVKISCKTSGHTFEYNMQWVKQSLGQSLEWIGGINPNNVGSIYNQKFRGKATL  
-----FR1----- CDR1 -----FR2----- CDR2 -----  
  
71            80            90            100          110  
TVDKSSSTAYMELRSLTSEDAVYYCARGYGNVAYWGQGTLVTVSA  
-----FR3----- CDR3 -----FR4-----

**B:**

1            10            20            30            40            50            60            70  
DIVMTQSQKFMSTSVDGRSVTCKASQNVTNVAWYQQKPGQSPKSLIYSASRYSGVPDRFTGSGSGTD  
-----FR1----- CDR 1 -----FR2----- CDR 2 -----  
  
71            80            90            100  
FTLTISNVQSEDLAEFFCQOYNRYPFTFGGGTKLELK  
-----FR3----- CDR 3 -----FR4---

**Figure 4**

EVQLQQSGPETGKPGASGKMSCKTSGHTSTEHNGWAKQSPGQSLEWIGGINPNNVGSI  
YNQKFRGKATLTADKSSSTAHMELRSPTSEDTAVYYCARGYGNVAYWGQGTLVTVSA

**Figure 5**

EVQLQQSGPETGKPGASGKMSCKTSGHTSTEHNGOWAKQSPGQSLEWNGGRNNSIVKSI  
TVSASGTKATLTADKSSSTAHMELRSPTSEDTAVYYCSPSYTYYRPGWGQGTLVTVSA

**Figure 6**

EVQLQQSGPETGKFATISFSCNTGYKLFGSTSGQWARQSPGQSLEWNGGRNNSIVKSI  
TVSASGTKATLTADKSSSTAHMELRSPTSEDTAVYYCSPSYTYYRPGWGQGTLVTVSA

**Figure 7**

EVQLQQSGPTLVKPTQTLTLSGFSFGSTSMNRLRQSPGQSLEWNGGRNNSIVKSI  
TVSASGTKATLTADKSSSTAHMELRSPTSEDTAVYYCSPSYTYYRPGWGQGTLVTVSA

**Figure 8**

DIQTTQSQKSQSTSAGDRASTTCASQNVSTNAAWYQQTPGQSPKSLIYAASSLQSGVP  
DRFTGSGSGTDFTQTTSNAQSEDSAEEFFCQQYNRYPHTFGGGTKLELK

**Figure 9**

DIQTTQSQKSQSTSAGDRASTTCTLLSVTRNDVAWYQQTPGQSPKSLIYAASSLQSGVP  
DRFTGSGSGTDFTQTTSNAQSEDSAEEFFCYLSGANLNLFGGGTKLELK

**Figure 10:**

1 KLTIESTPFN VAEGKEVLLL VHNLPQHLFG YSWYKGERVD GNRQIIGYVI GTQQATPGPA  
 61 YSGREIIYPN ASLLIQNIIQ NDTGFYTLHV IKSDLVNEEA TGQFRVYPEL PKPSISSNN  
 121 KPVEDKDAVA FTCEPEQTDA TYLWWVNQNS LPVSPRLQLS NGNRTLTLFN VTRNDTASYK  
 181 CETQNPVSAR RSDSVILNVL YGPDAPTISP LNTSYRSGEN LNLSCHAASN PPAQYSWFVN  
 241 GTFQOSTQEL FIPNITVNNS GSYTCAHNS DTGLNRTTVT TITVYAEPPK PFITSNNSNP  
 301 VEDEDAAVALT CEPEIQNTTY LWWVNQNQSLP VSPRLQLSND NRNLTLLSVT RNDVGPYECG  
 361 IQNELSVDHS DPVILNVLYG PDDPTISPSY TYYRPGVNLS LSCHAASNPP AQYSWLIDGN  
 421 IQQHTQELFI SNITEKNSGL YTCQANNSAS GHSRTTVKTI TVSAELPKPS ISSNNSKPVE  
 481 DKDAVAFTEC PEAQNTTYLW WVNGQSLPVs PRLQLSNGNR TLTLFNVTRN DARAYVCGIQ  
 541 NSVSANRSDP VTLDVLYGPD TPIISPPDSS YLSGANLNLS CHSASNPSHQ YSWRINGIPQ  
 601 QHTQVLFIAK ITPNNNGTYA CEVSNLATGR NNSIVKSITV SASGT

**Figure 11:**

1 DCGLPPDVNP AOPALEGRTS FPEDTVITYK CEEFSVKIPG EKDSVICLKG SQWS DIEEFC  
 61 NRSCEVPTRL NSASLKQPYI TQNYFPVGTv VEYECRPGYR REPSLSPKLT CLQNLKWSTA  
 121 VEFCKKKSCP NPGEIRNGQI DVPGGILFGA TISFSCNTGY KLFGSTSSFC LISGSSVQWS  
 181 DPLPECREIY CPAPPQIDNG IIQGERDHYG YRQSVTYACN KGFTMIGEHS IYCTVNNDEG  
 241 EWSGPPPECR GKSLTSKVPP TVQKPTTVNV PTTEVSPTSQ KTTTKTTTPN AQATRSTPVS  
 301 RTTKHFHETT PNKGSGTTSG TTRLLSGHTC FTLTGLLGTL VTMGLLT